

The predicted protein sequences of CssI (A), Hydrophobin (B), GAPDH-B (C), enolase (D), catalase B (E), catalase A (F), and isopropylmalate dehydrogenase B (G). X₁ is S or A and X₂ is L or I.

A
MLASFQFCILPRTYRLLCSAGAGPLLIQFVTVASALALAPTAVVARQGAAAFVTVNSIDVCPKKVAQEIIINPGPKVVTTP
YTCDQVKLGHLGDLVSYYNFDIEPLTKDTFPYCKALKVFDNEGCLGFPPLTWI PLESPLDKCIPEHYFSDEVKSI SFQLDCRE
DAPVKKPEYPGKEGAEQSAQAHEHSTKQDAQQGS HQQEVQNSPKQEARQGS RPAEAPKQEQAEEQASEAAPEKKASNPAD
SLGLGELTKVLGFR

B
VRFPVDDITVQKATEKCGDQAQLSCCNKATYAGDVTIDIEGILAGTLKNLIGGGSGTEGLGLFNQCSKLDLQSPIIGIPIQ
DLVNQCKQNIACCQNSPSDAVRFP

C
MATPKVGINGFGRIGRIVGLNSLSHGVDVAVNDPPIEVHYAAYMLKYDTTHGQFKGTIETYDQGLIVNGKKIRFYAEKD
PSQIPWSETGAAYIVESTGVFTTKEKASHLKGGAKKVIISAPSADAPMFVMGVNNTTYTSDIQVLSNACSTTNCLAPLA
KVINDKFGIVEGLMTTVHSYTATQKVVDAPSNDWRGGRATAQNIIPSSGTGAAGAVGKVI PSLNGKLTGMAMRVPTSNVS
VVDLTCRLEKGASYDEIKQAIKAASEEGELKNILGYTEDDVSSDLNGDERS SIFDAKAGISLNPNFVKLVAWYDNEW

D
MPISKIHARSVYDSRGNPTVEVDVATETGLHRAIVPSGASTGQHEAHEL RDGDKTQWGGKGVLKAVKNVNETIGPALIKENI
DVKDQSKVDEFLNKLDGTANKSNLGANAILGVSLAVAKAGAAEKGVPLYAHISDLAGTKKPYVLPVPFQNVNLNGGSHAGGRL
AFQEFMIVPDSAPSFSEALRQGALEVYQKLKALAKKKYQGSAGNVGDEGGVAPDIQTAEALDLITEAIEQAGYTGK
IKIAMDVASSEFYKADVKKYDLDFKNPESDPSKWLTYEQLADLYKSLAAKYPIVSIEDPFAEDDWEAWSYFYKTSDFQIVGD
DLTVTNPGRIKKAIELKSCNALLKVNQIGTLTESIQAAKDSYADNWGMVMSHRSGETEDVTIADIAGLRSQG IKTGAPCR
SERLAKLNQILRIEELGENTVYAGSKFR TAVNL

E
MRLTFIPSLIGVANAVCPYMTGELNRRDEISDGDAAAATEEFLSQYYLNDNDAFMTSDVGGPIEDQNSLSAGERGPTLLED F
IFRQKIQRFDHERVPERAVHARGAGAHGVFTSYGDFS NITAASFLAKEGKQTPVFVRVSTVAGSRGSSDLARDVHGFA TRFY
TDEGNFDIVGN NIPVFFIQDAILFPDLIHAVKPRGDNEIPQAATAHDSAWDFFSQQPSTMHTLLWAMSGHGI PRSF
RHVDGFGVHTFRFVTDGASKLVKFHWKSLQKASMWEEAQTSKGNPDFMRQDLHDAIEAGRYPEWELGVQIMDEEDQLR
FGFDLLDPTKIVPEEFVPIITKLGMQLNRNPRNYFAETE QVMFQPGHIVRGVDFTEDP LLQGR LFSYLD TQLNRHGGENFEQ
LPINQPRVPVHNNNRD GAGQMF IPLNPHAYS PKTSVNGSPKQANQTVGDGFF TAPGR TSGKLVRVAVSSSFEDVWS
QPRLPYNSLVPAEKQFVIDAIRFENANVKS P VVKNVVIQLNRIDNDLARRVARAIGVAEPEPDPTFFYHNKNTADVGTFG TK
LKKLDGLKVGVLGVSQHPGSGVEGASTLRDRLKDDGVDVVLVAERLADGVDQTYSTSDAIQF DAVVVAAGAESLFAASSFTG G
SANSASGASSLYPTGRPLQILIDGFRFGKTVGALGSGTAALRNAGIATSRDGVYVAQSVTDDFANDLKEGLRTFKF
LDRFPVDH

F
MATKIAGGLHRAQEV LQNTSSKSKKLVDLERDTADAHTQQLTTDHGVRVSN TDQWLRVTNDRRTGPSLLEDQIAREKIH RF
DHERI PERVVHARGTGAFGNFKLKESIEDLTYAGVLTDTSRNTFVVRVSTVQSGRGSADTVRDVRGFAVKFYTDEGNWDIV
GNNIPVFFIQDAVKFPDFVHAVKPEPHNEVPQAQTAHN NFWD FVYLHPEATHMFMWMSDRAIPRSYRMMQGFQGN
TFALVNKEGKRHFVKFHWI PHLGVHSLVWDEALKLGGQDDPDRKDLMEAI DNKAYPKWDFAIQV IPEEKQDDFEFDILDAT
KIWPENLVPLRVIGELELNRRNVDEFFPQTEQVAFCTSHIVPGIDFTDDP LLQGRNFSYFDTQISRLGINWEE LPINRPVCPV
LNHNRDGQMRHRITQGT VNYWPNRFEAVPPTGKSGVG GFTTYPQRVEGIKNRALNDKFRHEHNQAQLFYNSMS
EHEKLHMKAFS FELDHCDPTVYERLAGHRLAEIDLELAQKVAEMVGAPIPAKALKQNHGRRAPHL SQTEFIPKNPTIASR
RIAIIGDGYDPVASTGLKTAIKAASALPFIIGTKRS AIYATEDKTSKGIIPDHHYDGQRSTMF DATFIPGGPHVATLRQN
GQIKYWISETFGHLKALGATGEAVDLVKETLSGTLHVQVASSQSPEPVEWYG VVTAGGKQKPESFKESVQLKGAT
DFVGKFFYQISQHRNYQRELDGLASTIAF

G
MVTTYN I LVLPDGDIGPEVMT EAVKVLKVFENEHRKFNLRQELIGGCSIDAHGKS VTEEVKKAAL ESDAVLFAAVGGPKW
DHIRRLDGP EGGLQLRKAMDIYANLRPCSASSPSASIAKEFS PFQREVIEGVDFVVRENC GGAYFGKKIEEEDYAMD
EWGYSEREIQRITRLX₁ AEX₂ ALRHNPPW PVI SLDKANVLASSRLWRRVVEKTM TTEYPQVKLVHQ LADSASLILATNPRALN
GVILADNTFGDMISDQAGSIVGTLGLVLP SASLDGLPSETRKRTNGLYEP THGSAPT IAGQN IANP VAMILCVALMFRYSLDM
ETE AQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGDAI VAALQSS

FIGURE 1

BEST AVAILABLE COPY

The predicted antigenicity indices of Cssi (A) and hydrophobin (B) reisdues.

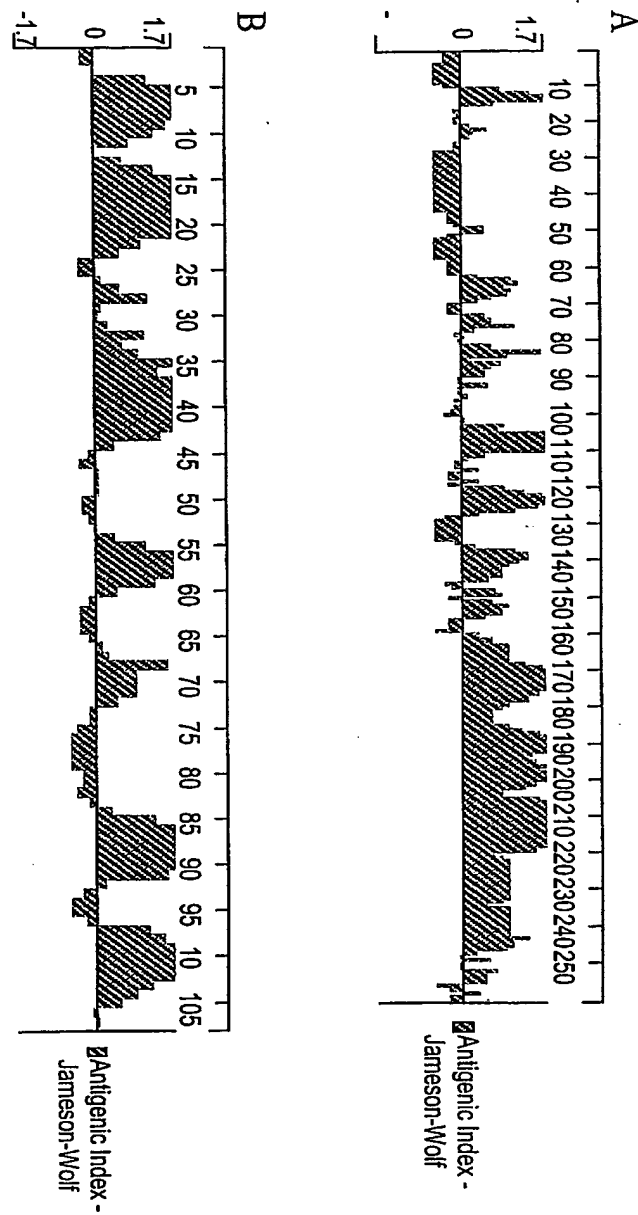


FIGURE 2

Alignment of the predicted protein sequences for GAPDH-A (Afa), GAPDH-B (Afb) and GAPDH-C (Afc).

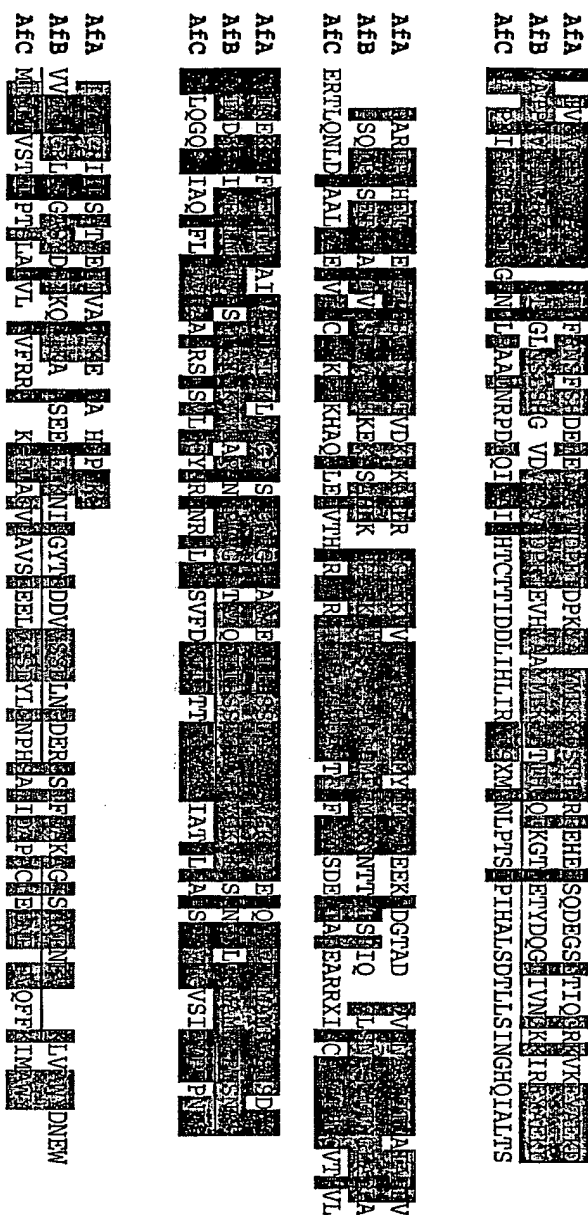


FIGURE 3

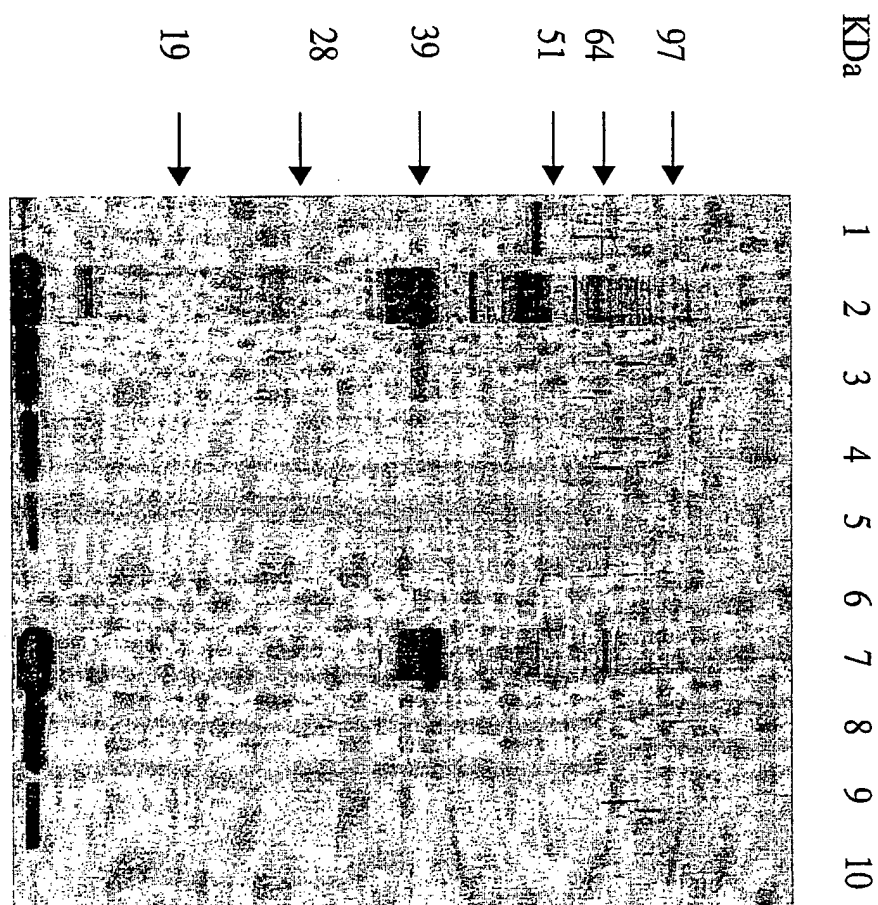


FIGURE 4

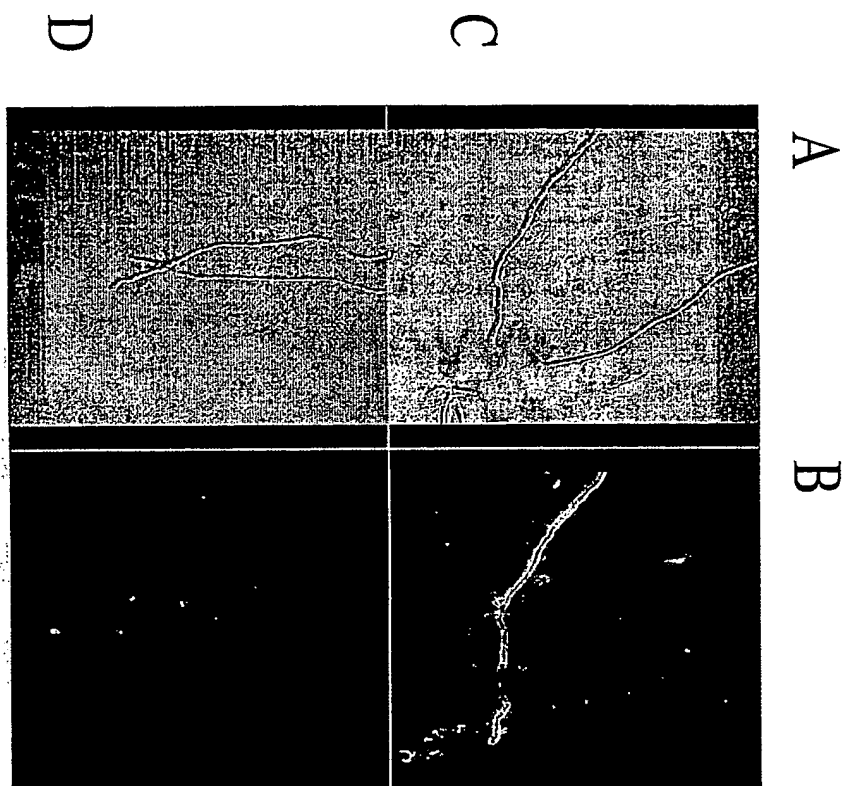


FIGURE 5

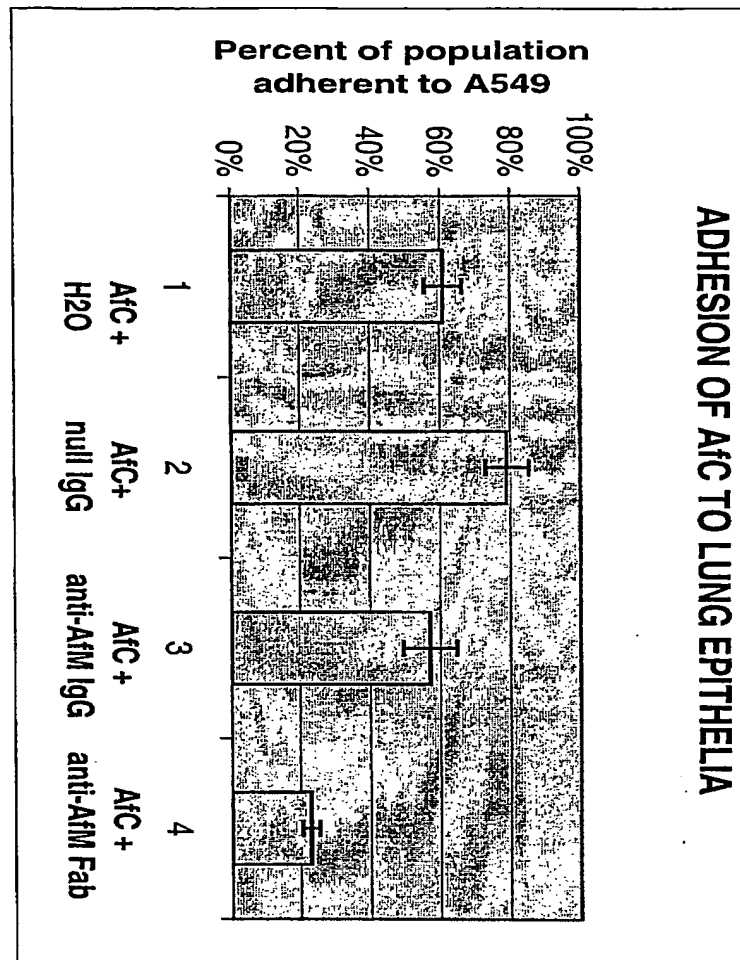


FIGURE 6

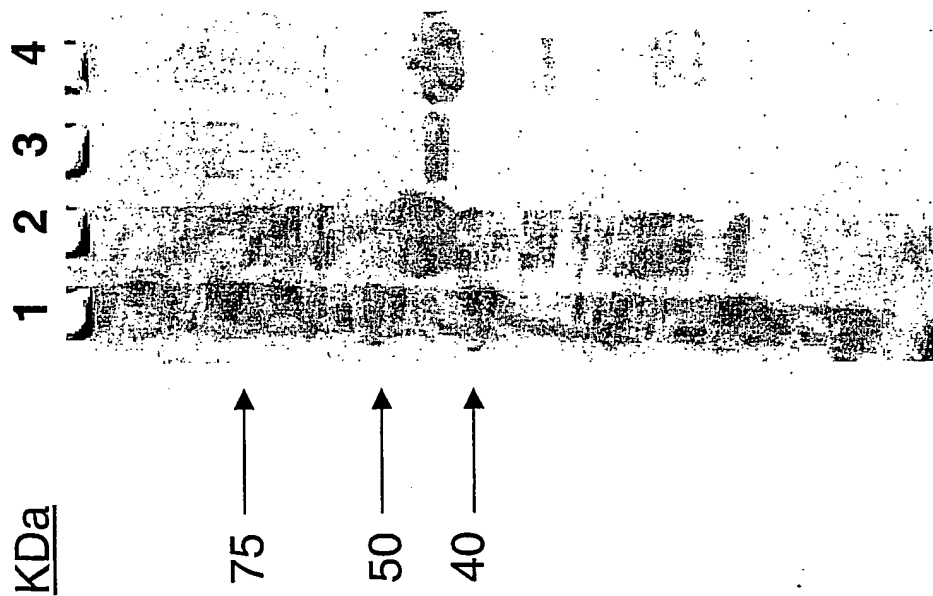


FIGURE 7

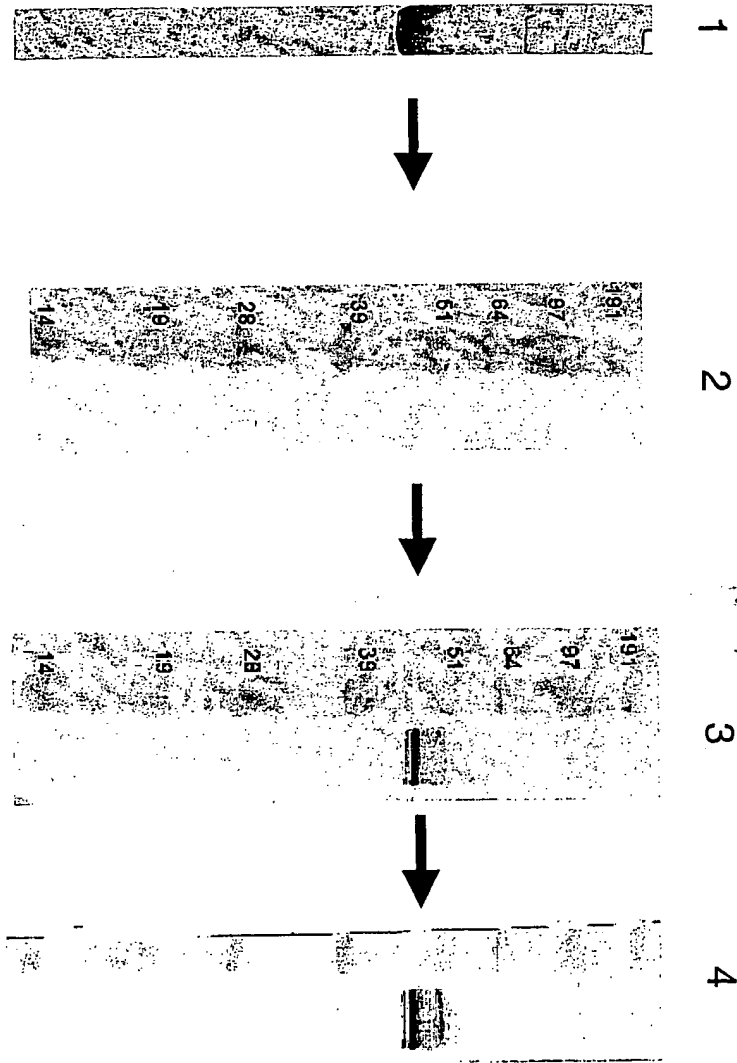


FIGURE 8

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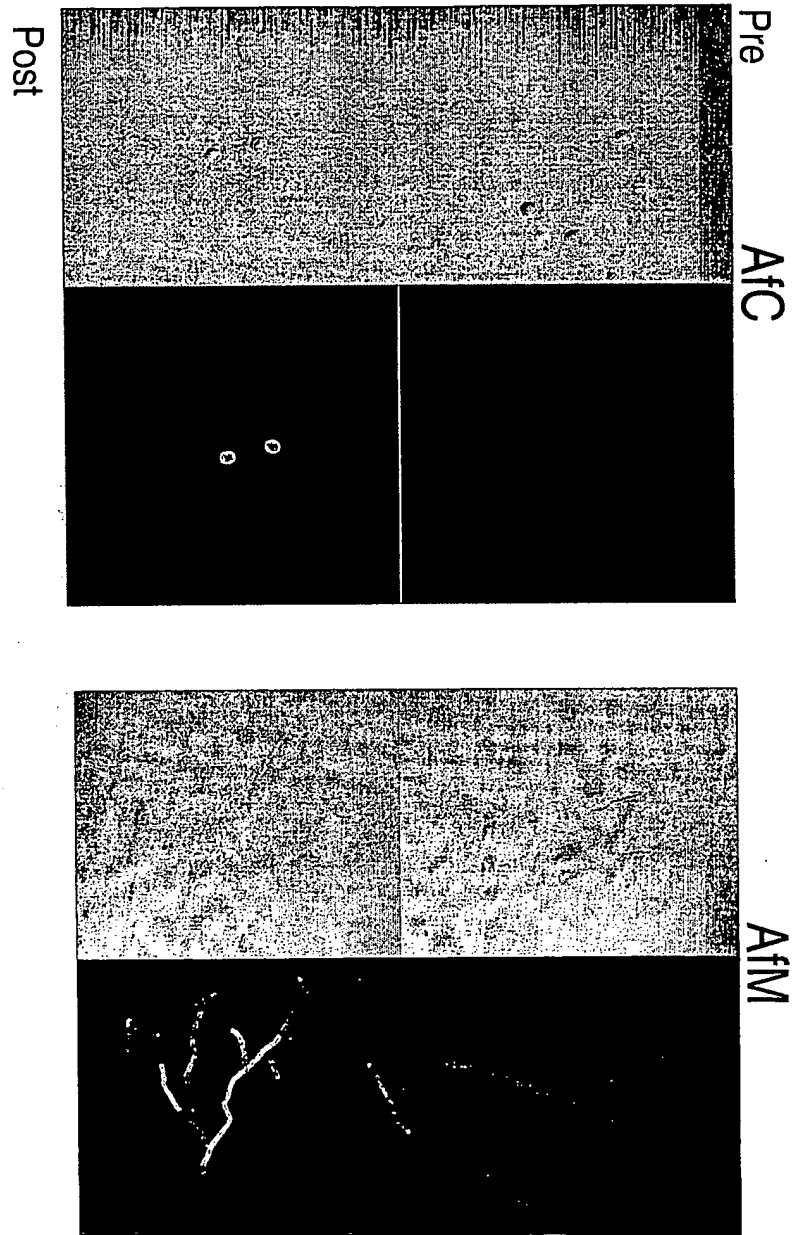


FIGURE 9

10/29

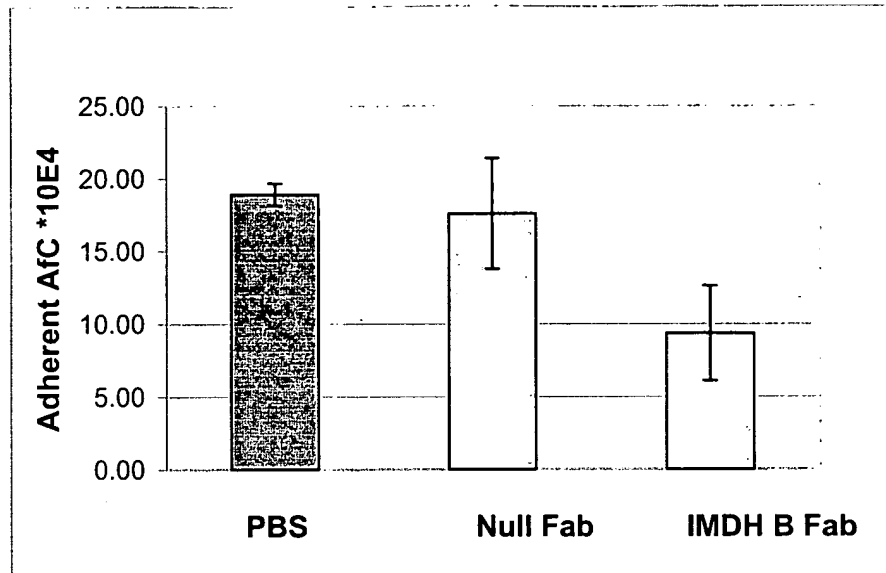


FIGURE 10

11/29

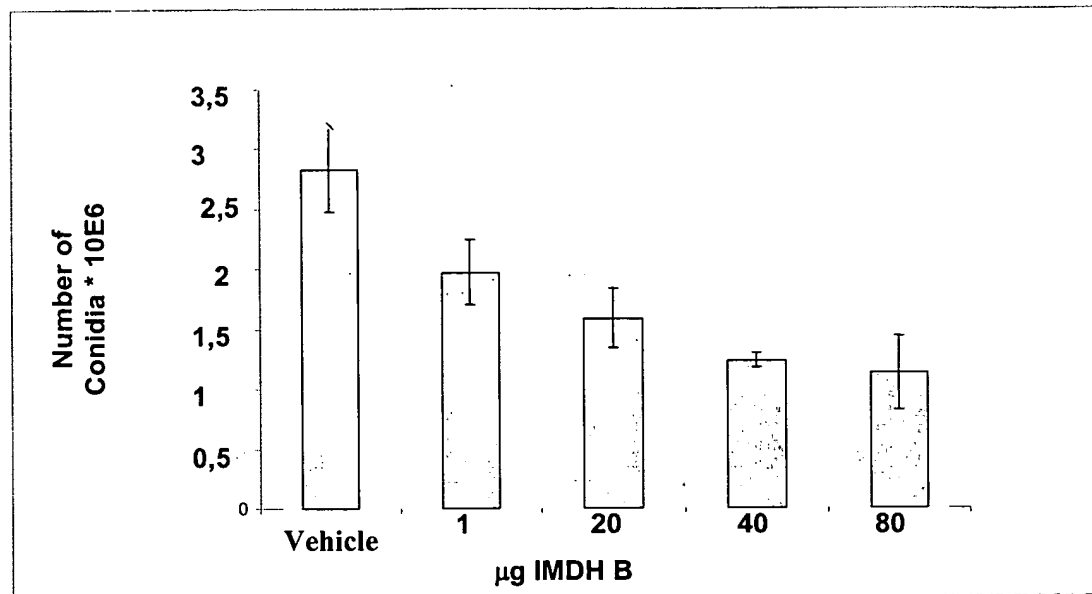


FIGURE 11

12/29

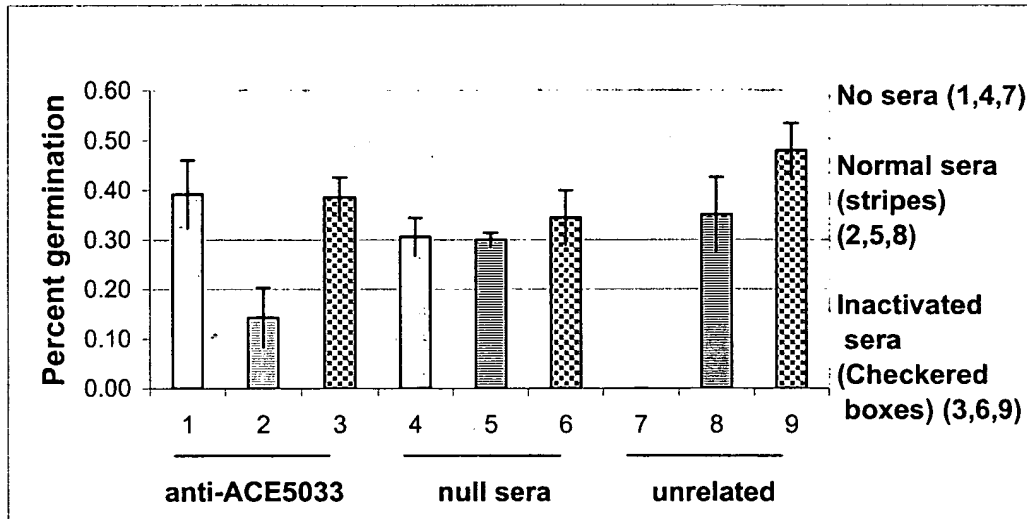
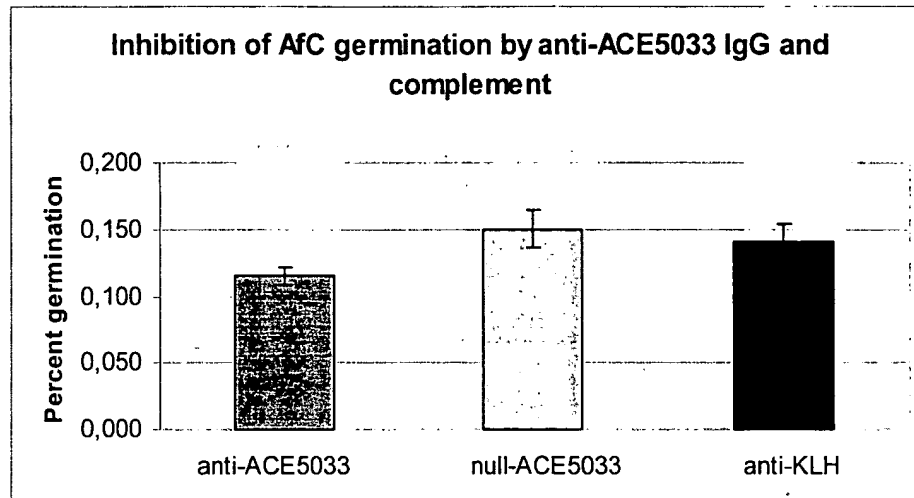


FIGURE 12

**FIGURE 13**

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IMDHB1: 3 SYNIVVFAGDHCGPEVSS-----VLRVIEKCRDDATFNLQDQLLGGVSSIDATGSPLTDEA 58
      +YNI+V GD GPEV + VL+V E + FNL+ +L+GG S IDA G +T+E
IMDHB2: 4 TYNILVLPDGGIGPEVMTEAVKVLKFEN--EHRKFNLRQELIGGCS-IDAHGKSVTEEV 60

IMDHB1: 59 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGLLRRLRKEMGTFGNLRPCNFAAPSLV-- 113
      AA +DAVL A+GGPKW G PE GLL+LRK M + NLRPC+ ++PS
IMDHB2: 61 KKAALSDAVLFAAVGGPKWDHIRRGLDGPPEGGLQLRKAMDIYANLRPCSASSPSASIA 120

IMDHB1: 114 -DGSPLRPEVCRGVDFNIIRELTGGIYFGDRKEDDGSGFAMDTEPYSRAEIERITRLAAH 172
      + SP R EV GVDF ++RE GG YFG + E++ +AMD YS EI+RITRL+A
IMDHB2: 121 KEFSPFRQEVIEGVDFVVRNCGGAYFGKKIEED--YAMDEWGYSEREIQRITRLSAE 178

IMDHB1: 173 LALQHNPPPLPVWSLDKANVLATSRLWRKTVTEVMAKEFPQLKVEHQLIDSAAMIMVKEPR 232
      +AL+HNPP PV SLDKANVLA+SRLWR+ V + M E+PQ+K+ HQL DSA++I+ PR
IMDHB2: 179 IALRHNPPWPVVISLDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATNPR 238

IMDHB1: 233 KLNGIVVTSNLFGDIISDEASVIPGSLGLLPSASLSGIP-DGKTKVNGIYEPHGSAPDI 291
      LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + + NG+YEP HGSAP I
IMDHB2: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSETRKRTNGLYEPHGSAPTI 298

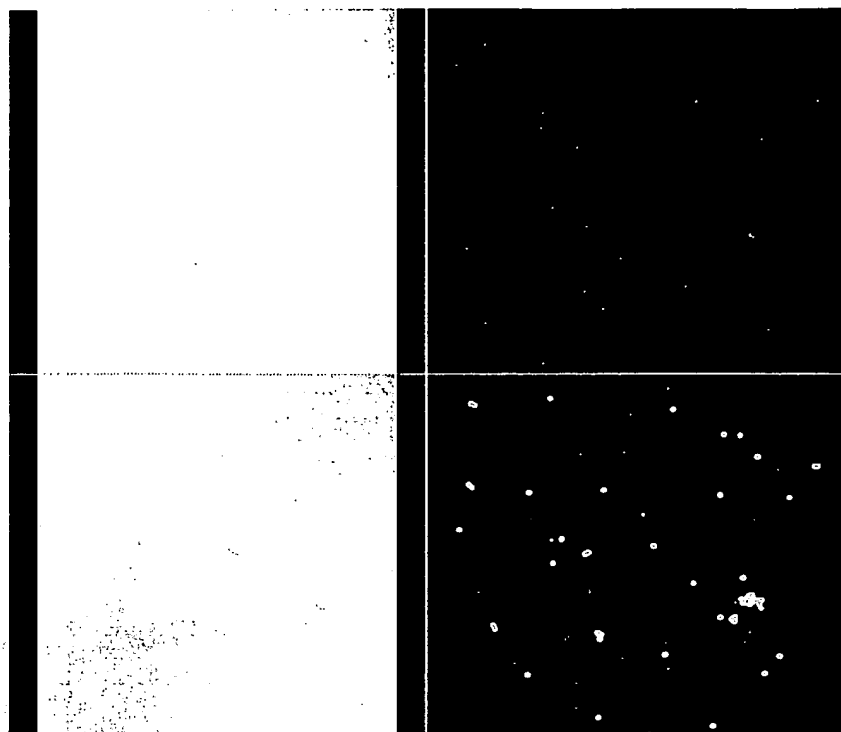
IMDHB1: 292 AGKGIVNPVAAILSVAMMMQYSLNRMDDARAIAETAVRNVIEAGIRTADIGGKSTTSEVGD 351
      AG+ I NPVA IL VA+M +YSL+ +A+ IE AV+ V++AGIRT D+GGKS T+EVGD
IMDHB2: 299 AGQNIANPVMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGD 358

IMDHB1: 352 AVAAELE 358
      A+ A L+
IMDHB2: 359 AIVAALQ 365

```

FIGURE 14

Afc



Afm

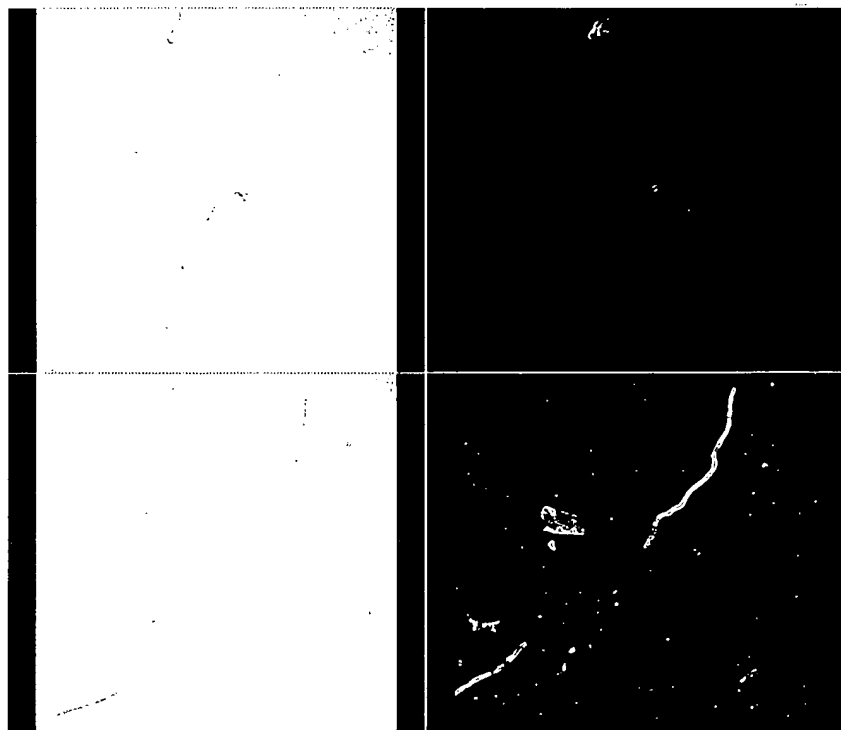


FIGURE 15

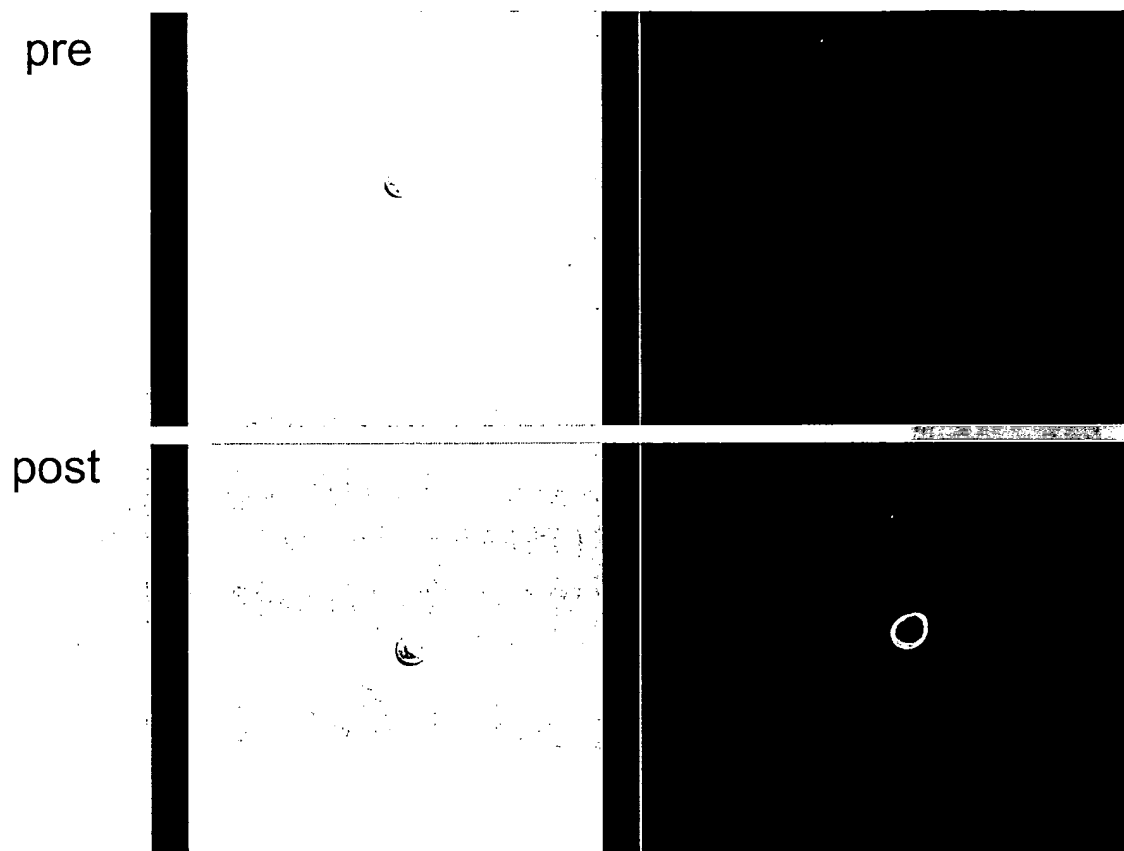


FIGURE 16

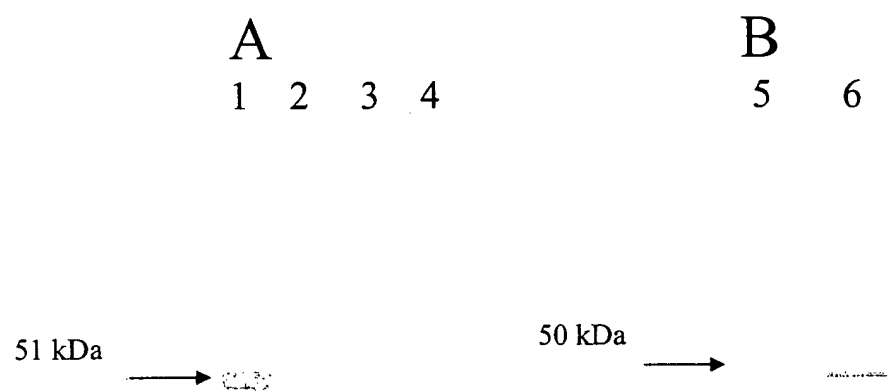


FIGURE 17

BLAST OF SEQ ID NO:36 AGAINST:

Candida orf:

>orf19.7080 orf10262:179916-178795:e 1122 bp, 373 aa, contig 244073 bp
 Length = 1122

Score = 335 bits (860), Expect = 1e-92
 Identities = 185/368 (50%), Positives = 246/368 (66%), Gaps = 9/368 (2%)
 Frame = +1

Query: 2 VTTYNILVLPDGGIGPEVMTEAVKVLKFEN----EHRKFNLRLQELIGGCSIDAHGKSVT 57
 V T I VLPD +G E++ EA+KVLK E + +F+ + LIGG +IDA G +
 Sbjct: 7 VKTKTITVLPGDHVGTEIVNEAIKVLKAIEAATPYQKIQFDFKHHLIGGAIDATGVPLP 186

Query: 58 EEVKKAALESDAVLFAAVGGPKWDHIRGLDGPGEGLLQLRKAMDIYANLRPCSASSPSA 117
 ++ ++A SDAVL AVGGPKW G PE GLL++RK +++YAN+RPC+ +S S
 Sbjct: 187 DDALESASKSSDAVLLGAVGGPKWG---TGTVRPEQGLLKIRKELNLYANIRPCNFASDSL 357

Query: 118 SIAKEFSPFRQEVIEGVDFVVRVRENCGGAYFGKKIEEEDY-----AMDEWGYSEREIQRI 172
 E SP + EV++G + ++VRE GG YFG++ E+E+ A D Y+ E+ RI
 Sbjct: 358 L---ELSPLKAEVVKGTNLIIVRELVGGIYFGERQEQEESDKKTAWDTEKYTVDEVTRI 528

Query: 173 TRLSAEIALRHNPWPVISLDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLI 232
 TR++A +AL+HNPP P+ SLDKANVLASSRLWR+ V+K ++ E+P + + HQL DSA++I
 Sbjct: 529 TRMAAFMALQHNPPLPIWSLDKANVLASSRLWRKTVDKVISEEFPAHSVQHQLIDSAAMI 708

Query: 233 LATNPRLNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPH 292
 L NP LNG+I+ N FGD+ISD+A I G+LG+LPSASL LP GLYEP H
 Sbjct: 709 LIQNPTKLNGLIITSNMFGDIISDEASVIPGSLGLLPSASLASLPD--TNTAFGLYEPCH 882

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
 GSAP + N NP+A IL A M R SLD EA+ +E+AV+ VLD+GIRT DL G S
 Sbjct: 883 GSAPDLPA-NKVNPIATILSAASMLRLSLDCVKEAEAEAEAVKQVLDGIRTDLRGTSS
 1059

Query: 353 TNEVGDAI 360
 T EVGDAI
 Sbjct: 1060TTEVGDAI 1083

Candida seq orf10262:179916-178795**1**

VKTKTITVLPGDHVGTEIVNEAIKVLKAIEAATPYQKIQFDFKHHLIGGAIDATGVPLPDDALESASKS
 SDAVLLGAVGGPKWGTGTVRPEQGLLKIRKELNLYANIRPCNFASDSLLELSPLKAEVVKGTNLIIVRE
 LVGGIYFGERQEQEESDKKTAWDTEKYTVDEVTRITRMAAFMALQHNPPLPIWSLDKANVLASSRLWR
 KTVDKVISEEFPAHSVQHQLIDSAAMILIQNPTKLNGLIITSNMFGDIISDEASVIPGSLGLLPSASLA
 SLPDTNTAFGLYEPCHGSAPDLPANKVNPIATILSAASMLRLSLDCVKEAEAEAEAVKQVLDGIRTDLRGTSS
 LRGTTSS1060TTEVGDAI

FIGURE 18

BLAST OF SEQ ID NO:36 AGAINST:

Elrond pep

A. nidulans

>AnrP4374925 LE3B_ASPNG 3-isopropylmalate dehydrogenase B (Beta-IPM

dehyd

Length = 370

Score = 597 bits (1540), Expect = e-171

Identities = 295/364 (81%), Positives = 326/364 (89%), Gaps = 1/364 (0%)

Query: 4 TYNILVLPDGGIGPEVMTEAVKVLKVFENEHRKFNLQELIGGCSIDAHGKSVTEEVKKA 63
 +YNILVLPDGGIGPEVM EA K+L +F +F + ELIGGCSID HGKSVT+ V A
 Sbjct: 5 SYNILVLPDGGIGPEVMAEATKILSLFNTSTVRFRTQTELIGGCSIDTHGKSVTQAVLDA 64

Query: 64 ALESDAVLFAAVGGPKWDHIRRGLDGPGEGLLQVRKAMDIYANLRPCSASSPSASIAKEF 123
 A+ SDAVLFAAVGGPKWDHIRRGLDGPGEGLLQ+RKAMDIYANLRPCS SPS IA++F
 Sbjct: 65 AVSSDAVLFAAVGGPKWDHIRRGLDGPGEGLLQVRKAMDIYANLRPCSVDSPSREIARDF 124

Query: 124 SPFRQEVIEGVDFVVRVRENCGGAYFGKKIEEDYAMDEWGYSEIEIQRITRLSAEIALRH 183
 SPFRQ+VIEGVDFVVRVRENCGGAYFGKK+EE+DYAMDEWGYE EIQRITRLSAE+ALRH
 Sbjct: 125 SPFRQDVIEGVDFVVRVRENCGGAYFGKKVEEDYAMDEWGYSEIEIQRITRLSAELALRH 184

Query: 184 NPPWPVISLIDKANVLASSRLWRRVVEKTMTEYPPQVKLVHQLADSASLILATNPRLNGV 243
 +PPWPVISLIDKANVLASSRLWRRVVEKTM+ EYPQVKLVHQLADSASLI+ATNPRLNGV
 Sbjct: 185 DPPWPVISLIDKANVLASSRLWRRVVEKTMSEYPPQVKLVHQLADSASLIMATNPRLNGV 244

Query: 244 ILADNTFGDMISDQAGSIVGTGLVLPASLDGLPSE-TRKRTNGLYEPHGSAPTIGQN 302
 ILADNTFGDM+SDQAGS+VGTGLVLPASLDGLP +++ +GLYEPHGSAPTIG+N
 Sbjct: 245 ILADNTFGDMVSDQAGSLVGTGLVLPASLDGLPKPGEQRKVHGLYEPHGSAPTIGKN 304

Query: 303 IANPVAMILCVALMFRYSIDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGDAIVA 362
 IANP AMILCVALMFRYS +ME EA++IE AV+ VLD GIRT DLGG +GT E GDA+VA
 Sbjct: 305 IANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTSIDLGGSTGTREFGDAVVA 364

Query: 363 ALQG 366
 AL+G
 Sbjct: 365 ALKG 368

>AnrP4374925 niger seq

MSEKSYNILVLPDGGIGPEVMAEATKILSLFNTSTVRFRTQTELIGGCSIDTHGKSVTQA
 VLDAAVSSDAVLFAAVGGPKWDHIRRGLDGPGEGLLQVRKAMDIYANLRPCSVDSPSREI
 ARDFSPFRQDVIEGVDFVVRVRENCGGAYFGKKVEEDYAMDEWGYSEIEIQRITRLSAEL
 ALRHDPPWPVISLIDKANVLASSRLWRRVVEKTMSEYPPQVKLVHQLADSASLIMATNPRA
 LNGVILADNTFGDMVSDQAGSLVGTGLVLPASLDGLPKPGEQRKVHGLYEPHGSAPTIG
 AGKNIANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTSIDLGGSTGTREFGD
 AVVAALKGEL

FIGURE 19

BLAST OF SEQ ID NO:36 AGAINST:

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┌   BLASTP:temp job2 pep 6 AnrP3711474
>AnrP3711474 hypothetical protein [Aspergillus oryzae]
    Length = 364

Score = 375 bits (963), Expect = e-104
Identities = 195/367 (53%), Positives = 260/367 (70%), Gaps = 10/367 (2%)

Query: 2   VTTYNILVLPDGGIGPEVMTEAVKVLKVFE-NEHRKFNLQELIGGCSIDAHGKSVTEEV 60
          +++YNI+V  GD  GPEV  EA+KVL+  E N   FNL+  L+GG SIDA G  +T+E
Sbjct: 1   MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNRDVTFNLQDHLGGASIDATGSPLTDEA 60

Query: 61   KKALESDAVLFAAVGGPKWDHIRRLDGPPEGGLQLRKAMDIYANLRPCSASSPSASIA 120
          AA  +DAVL  A+GGPKW      G   PE G+L+LRK M  + NLRPC+ ++PS
Sbjct: 61   LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLV-- 115

Query: 121  KEFSPFRQEVIEGVDFVVRVRENCGGAYFGKKIEEED--YAMDEWGYSEREIQRITRLSAE 178
          E SP R +V  GV+F ++RE  GG YFG++ E++  YAMD  YS  EI+RI RL+A
Sbjct: 116  -ESSPLRADVCRGVNFNIIRELTGGIYFGERKEDDGSYGAMDTPEYSRAEIERIIRLAH 174

Query: 179  IALRHNPPWPVISLIDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATNPR 238
          +AL+H+PP PV SLDKANVLA+SRLWR+VV + M  E+PQ+K+ HQL DSA++I+  NPR
Sbjct: 175  LALQHDPPPLPVWSLIDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPR 234

Query: 239  ALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPHGSAPT I 298
          LNG+++  N FGD+ISD+A  I G+LG+LPSASL G+P +  + NG+YEP HGSAP I
Sbjct: 235  QLNGIVVTSNLFGDIISDEASVIPGSLGLLPSASLSGIP-DGNSKVNGIYEPHGSAPDI 293

Query: 299  AGQNIANPVMILCVLDMETEAQRIEKAVQGVLDA GIRT PDLGGKSGTNEVGD 358
          AG+ I NPVA IL VA+M +YS  +  EA+ IE+AV  V+++G+RT D+GGK+ T EVGD
Sbjct: 294  AGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGD 353

Query: 359  AIVAALQ 365
          A+ A L+
Sbjct: 354  AVAAELE 360

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Oryzae seq >AnrP3711474
MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNRDVTFNLQDHLGGASIDATGSPLTDEA
LNAAKNADAVLLGAIGGPKWGTGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLVESSPL
RADVCRGVNFNIIRELTGGIYFGERKEDDGSYGAMDTPEYSRAEIERIIRLAH LALQHD
PPLPVWSLIDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLNGIV
VTSNLFGDIISDEASVIPGSLGLLPSASLSGIPDGNSKVNGIYEPHGSAPDIAGKGIVN
PVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGD AVAAELE
LLK

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FIGURE 20

BLAST OF SEQ ID NO:36 AGAINST:

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┌ BLASTP:temp_job2_pep_9_AnP4379986
>AnP4379986 conserved hypothetical protein [Aspergillus nidulans
  FGSC A4
  Length = 357

Score = 149 bits (376), Expect = 1e-36
Identities = 113/369 (30%), Positives = 186/369 (49%), Gaps = 27/369 (7%)

Query: 1  MVTTYNILVLPDGDGIGPEVMTEAVKVLKFENEHRKFNLRQELIGGCS--IDAHGKSVTE 58
          M  TY I  +P DGIGPEV+   V VLK  ++ + F+L    +   S   A GK + +
Sbjct: 1  MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDWSSETFKATGKYIPD 60

Query: 59  EVKKAALLESDAVLFAAVGGPKW-DHIRRLDGPPEGGLQLRKAMDIYANLRPCSASSPSA 117
          +   ++DA+LF AVG P   DHI          G  L + +   YAN+R      P+
Sbjct: 61  GGLEVLKKNDAILFGAVGAPDVPDHISLW-----GLRLAICQPFQQYANVR-----PTR 109

Query: 118  SIAKEFSPFRQEVIEGVDFVVVRENCGGAYFGK-----KIEEEDYAMDEWGYSEREIQRI 172
          +   SP R+   +D+V+VREN  G Y G+   +   + A +   +S + ++RI
Sbjct: 110  VLRGTQSPLRKCNTGDLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVERI 169

Query: 173  TRLSAEIALRHNPWPFPVISLDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLI 232
          R + E A + P   + + K+N   + +   V   + ++P+V +   L D+ +
Sbjct: 170  MRFAFETAAK-RPRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTR 228

Query: 233  LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPH 292
          +   P +L+  I+A N   D++SD A ++ G++G+ P+++LD      ++   ++EP H
Sbjct: 229  MVLKPESLD-TIVASNLHADILSDLAALAGSIGIAPTSNLD-----PTRQNPSMFEPH 282

Query: 293  GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDA GIRTPDLGGKSG 352
          GSA  I G+ IANPVA   A M + L + A ++ + V+ V ++GI T DLGG +
Sbjct: 283  GSAFDITGKGIANPVATFWTAAEMLEW-LGEKDAADKLMQCYESVCESGILTADLGGTAT 341

Query: 353  TNEVGDAIV 361
          T EV  A+V
Sbjct: 342  TKEVTSADV 350

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```

Nidulans seq >AnP4379986
MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDWSSETFKATGKYIPD
GGLEVLKKNDAILFGAVGAPDVPDHISLWGLRLAICQPFQQYANVRPTRVLRGTQSPLRK
CNTGDLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVERIMRFAFETAAKR
PRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTRMVLKPESLDTIV
ASNLHADILSDLAALAGSIGIAPTSNLDPTRQNPSMFEPHGSADFITGKGIANPVATF
WTAAEMLEWLGEKDAADKLMQCYESVCESGILTADLGGTATTKEVTSADVVEINRLN

```

FIGURE 21

BLAST OF SEQ ID NO:36 AGAINST:

>gnl|TIGR_222929|contig:1772:c_posadasii Coccidioides posadasii C735
 unfinished fragment of genome
 Length = 119053

Score = 286 bits (732), Expect(2) = e-128
 Identities = 146/233 (62%), Positives = 173/233 (74%), Gaps = 24/233 (10%)
 Frame = -3

Query: 160 AMDEWGYSTTEIQXXXXXXXXXXXXHDPWPVISLTKANVLASSRLWRRVVENTISVEYP 219
 AMDEWGYST E+Q HDPPWPVIS+DKANVLASSRLWRRVVE T++ E+P
 Sbjct: 33806 AMDEWGYSTQEVQRIARLAHVALRHDPWPVISMDKANVLASSRLWRRVVEKTLTTEFP
 33627

Query: 220 QVKLVHQLADSASLIMATDPRLNGVILADNTFGDMLSDQAGSLIGTLGVLPSASLDGLP 279
 QVK HQLADSASLIMAT+PR LNGV+LADNTFGDMLSDQAGS++G+LGVLPSASL G+P
 Sbjct: 33626 QVKFSQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPSASLSGIP
 33447

Query: 280 HPGKQE--KVRGLYEPTHGSAPT-----IAGKNIANPTAMILC 315
 +++ K LYEPTHGSAPT IAGKN+ANP AMILC
 Sbjct: 33446 GEKRKDGKKSALYEPTHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 33267

Query: 316 VSLMFRYSFNMENEARQIEDAVRAVLDRGLRTPDLGGNSSTQEFDAVVAALQ 368
 V++MFRYSFNME EA+ IE+AV A L+ G+RTPDLGG + T + G+A+VA ++
 Sbjct: 33266 VAMMFRYSFNMEPEAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHK 33108

Query: 4 TRAYNILVLPDGGIGPEVMAEAIKVLRTFNSSSMQFHLQEELIGGISIDTHGHSVTQPXX 63
 ++ YNIL LPGDGIGPE+MAEAIKVL+ F+S ++ F+L+ ELIGG SLD HG +T
 Sbjct: 34383 SKTYNILTLPDGGIGPEIMAEAIKVLQAFSSPNLNFNLRELIGGCSIDAHGTPITDAVK
 34204

Query: 64 XXXXXXXXXXXXXXXGSKVDHIRGLDGPPEGGLLQVRKAMDIYANLRPCSVDVPSREIAR 123
 GG K D RRGL+GPEGGLLQ+RK +D+Y N+RPCS DV ++R
 Sbjct: 34203 QAALESDAVLFAVGGPKWDSSRRGLEGPPEGGLLQLRKVLVDVYGNVRPCSTDV-CASVSR
 34027

Query: 124 DFSPFRQEVIEGVDFVVRVRENCGAYFGKKVEEENY 159
 +FSP+R EV+EGVDFVV+RENCGAYFGK VE+E+Y
 Sbjct: 34026 EFSPYRTEVVEGVDFVVRVRENCGAYFGKXVEDEDY 33919

Coccidioides

2

SKTYNILTLPDGGIGPEIMAEAIKVLQAFSSPNLNFNLRELIGGCSIDAHGTPITDAVKQAALESDAVLFAVGGPKWDSSRRGLEGPPEGGLLQLRKVLVDVYGNVRPCSTDVCASVSREFSPYRTEVVEGVDFVVRVRENCGAYFGKXVEDEDYAMDEWGYSTQEVQRIARLAHVALRHDPWPVISMDKANVLASSRLWRVVEKTLTTEFPQVKFSQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPSASLSGIPGEKRKDGKKSALYEPTHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILCVAMMFRYSFNMEPEAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHK

FIGURE 22

SEQ ID NO:36 against: Cryptococcus >chr01b.b3501.031220.C11
(289426 bp) Length = 289426

Score = 183 bits (465), Expect(3) = 3e-68 Frame = +3
Identities = 113/258 (43%), Positives = 144/258 (55%), Gaps = 39/258 (15%)

Query: 148 FGKKIE--EEDYAMDEWGYSEREIQRITRLSAEIALRHNPPFWFVISLDRKANVLASSRLWR 205
FG++ E +E A D+ YS+ EI+RITR++A+IAL PP P+ S+DRKANVLA+SRLWR
Sbjct: 173334 FGERQETNDEGVAWDQCIYSKPEIERITRVAAQIALAAEPPLPITSVDKANVLATSRLWR 173513

Query: 206 RVVEKTMTEYPQVKLVHQLADSASLILATNPRALNGVILADNTFGDM----- 253
+ V + M EYPQ+KL HQL DSA++I+ NPR LNGV+L +N FGDM
Sbjct: 173514 KTVSELMAKEYPQLKLEHQLVDSAAIMIMIANPRKLNGLVLLTENMFGDM*VLSMVTKYRC* 173693

Query: 254 -----ISDQAGSIVGTGLGVLPASLDGLPSETRKRTNGLYE-----PTHGS 294
S A + L + P LP ++ HGS
Sbjct: 173694 VCVVFLTRAPSSPAPLVSSLLRLSPVPPITLSLPFWVSMSRTSIFPFLTYFN*PLCSIHGS 173873

Query: 295 APTIAGQNIANFVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAG-----IRTPDLG 348
AP IAGQ IANP+ IL A+M RYSL EA IE+AVQ VLD+ RT DLG
Sbjct: 173874 AFDIAGQGIANPIGTILSAAMMLRYSLGKREAAIEQAVQKVLDASAESGGFDYRTKDLG 174053

Query: 349 GKSGTNEVGDAIVAALQG 366
G+ T EVGD +V L+G
Sbjct: 174054 GQRSTKEVGDKVVEVLKG 174107

Query: 15 IGPEVMTAEAVKVLKVFENEHR-KFNLRQELIGGCSIDAHGKSVTEEVKKALESDAVLFA 73
IGPEV+ EAV+VL+ N K +L+ GG +ID HG + +E KA E+DAVL
Sbjct: 172844 IGPEVVAEAVRVLETIVNHSDDLKLDLKSDFGGAAIDNHGVPLPDETLLKACREDAVLMG 173023

Query: 74 A-----VGGPKWDHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPS 116
A VGGPKW G PE G+L+LRK + +YAN+RP A+ S
Sbjct: 173024 ACDFLAIRIKS*TA*KGSVGGPKWGV---GPVRPEQGILKRLKELGLYANIRP--ANFAS 173188

Query: 117 ASIAKEFSPPRQEVIEGVDFVVVRENCGG 145
S+ K SP +++ G D +V+RE GG
Sbjct: 173189 ESLLKR-SPLKEDTARGTDIIVLRELIGG 173272

Query: 244 ILADNTFGDMISDQAGSIVGTGLGVLPASLD-----GLPS---ETRRKRTNGLYEPH 292
+L + +GD++SD + ++G LG+ PS ++ G PS K ++E H
Sbjct: 238292 LLIPHRYGDILSDLSAGLIGGLTSPSGNIGKVSLSHDYGPSIELTGDK*DA SIFEAVH 238471

Query: 293 GSAPTIAGQNIANFVAMILCVALMFR----- 318
GSAP I G+ +ANP A++L +M R
Sbjct: 238472 GSAPDIEGKGLANPTALLSSLMMLR*VTQIPSVIVPALYSPVPDHTHPLARNVADLFVH 238651

Query: 319 YSLDMETEAQRIEKA---VQG-----VLDAGIRTPDLGGKSGTNEVG 358
+ + A +IEKA V G + + T DLGGK+GT E D
Sbjct: 238652 RHMSLYELADKIEKAALSVSGTFWLFHTFEMLIQVS*TIAEGKAITRDLGGKAGTKEYTD 238831

Query: 359 AIVAAL 364
AI++ L
Sbjct: 238832 AILSKL 238849

Query: 95 LQLRKAMDIYANLRPCSASSPSASIAKEFSPPRQEVIEGVDFVVVRENCGGAYFGKKIEE 154
L LR+ ++AN+RPC SI +P+ + V+ V++REN G Y G IE
Sbjct: 237609 LTLRRTFSLEFANVRPC-----VSIKGYKTPY-----DNVNTVLIRENTEGEYSG--IEH 237749

Query: 155 E 155
E
Sbjct: 237750 E 237752

Query: 5 YNIVLPGDGIGPEVMTAEAVKVLK 28
Y + ++PGDGIGPE+ ++ K
Sbjct: 237256 YTVTLIPGDGIGPEIANSVKQIFK 237327

Query: 4 TYNIVLPGDGIG 16
++ I VLPDGIG
Sbjct: 172752 SFKITVLPDGIG 172790

FIGURE 23

Clustalw of sequences of figure 18-22

```

! Sequence: BLASTP:temp_job2_pep_4_AnRP4374925  nidulans (see figure 19)
! Sequence: BLASTP:temp_job2_pep_6_AnRP3711474  oryzae (see figure 20)
! Sequence: BLASTP:temp_job2_pep_9_AnRP4379986  nidulans (see figure 21)
! Sequence: USERPROTEIN:1_job6_1  candida (see figure 18)
! Sequence: USERPROTEIN:2_job7_2  coccidioides (see figure 22)
CLUSTAL W (1.82) multiple sequence alignment

temp_job2_pep_4_AnRP4374925  ---SYNILVLPDGDGIGPEVMAEATKILSLFNTST---VRFRTQTELIGG
temp_job2_pep_6_AnRP3711474  -MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNR---DVTFNLDHLLGG
temp_job2_pep_9_AnRP4379986  MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQS--FSLDFTHLDWSS
1_job6_1  -VKTKTITVLPGDHVGTEIVNEAIKVLKAIEAATPYQKIQFDFKHHLLIGG
2_job7_2  -SKTYNILTLPDGDGIGPEIMAEAIKVLQAFSSPN----LNFNLRNELIGG
      :  *  .:  .*  *.:  .  :*  .  .  :  ..

temp_job2_pep_4_AnRP4374925  CSIDTHGKSVTQAVLDAVSSDAVLFAAVGGPKWDHIRRGLDGPPEGGLLQ
temp_job2_pep_6_AnRP3711474  ASIDATGSPLTDEALNAAKNADAVLLGAIGGPKWG---TGAVRPEQGILK
temp_job2_pep_9_AnRP4379986  ETFKATGKYIPDGGLEVLKKNDAILFGAVGAPDVP---DHISLWGLRLA
1_job6_1  AAIDATGVPLPDDALESAKSSDAVLLGAVGGPKWG---TGTVRPEQGILLK
2_job7_2  CSIDAHGTPITDAVKQAALSDAVLFASVGGPKWDSSRRGLEGPPEGGLLQ
      :::  *  :::  :  .  **:*:::*.*.  .  *

temp_job2_pep_4_AnRP4374925  VRKAMDIYANLRPCSVDSPSREIARDFSPFRQDVIEGVDFVVVRENCGGA
temp_job2_pep_6_AnRP3711474  LRKEMGTFGNLRPCNFAAPSL---VESSPLRADVCRGVNFNIIIRELTGGI
temp_job2_pep_9_AnRP4379986  ICQPFQQYANVRPTRVLRGTQ-----SPLRKCNTGDLDWVIVRENSEGE
1_job6_1  IRKELNLYANIRPCNFASDSL---LELSPLKAEVVKGNTNLIIVRELVGGI
2_job7_2  LRKVLDDVYGNVRPCSTDVCCAS-VSREFSPYRTEVVEGVDFVVLRENCGGA
      :  :  :  .:.*:**  :  **  :  .  :  ::**  *

temp_job2_pep_4_AnRP4374925  YFG-----KKVEEDDYAMDEWGYSAIEIQRITRLSAELALRHDPWPVIS
temp_job2_pep_6_AnRP3711474  YFGERKEDDGSG---YAMDTEPYSRAEIERIIRLA AHLALQHDPPLPVWS
temp_job2_pep_9_AnRP4379986  YAGQGGRSHRGHPWEVATEVAIFSRQGVERIMRFAFETA AAKR-PRKLLTV
1_job6_1  YFGERQE QEESEDKKTAWDTEKYTVDEVTRITRMAAFMALQHNPLPIWS
2_job7_2  YFG-----KXVEDEDYAMDEWGYSTQEVQRIARLA AHVALRHDPWPVIS
      *  *  .  *  :  ::  :  **  *::  *  ::  *  :

```

FIGURE 24

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

LDKANVLASSRLWRRVVEKTMSEEYPQVKLVHQLADSASLIMATNPRLN
LDKANVLATSRLWRKVVEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLN
VTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTRMVLKPESLD
LDKANVLASSRLWRKTVDKVISEEFPALSVQHQLIDSAAMILIQNPTKLN
MDKANVLASSRLWRRVVEKTLTTEFPQVKFSHQLADSASLIMATNPRLN
: * : * . . : * : : : * : . : * * : : : : * * :

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

GVILADNTFGDMVSDQAGSLVGTGLGVLPSASLDGLP--KPGEQRKVHGLY
GIVVTSNLFGLDIISDEASVIPGSLGLLPSASLSGIP----DGNSKVNGIY
-TIVASNLHADILSDLAAALAGSIGIAPTSNLDPTR-----QNPSMF
GIIITSNMFGDIISDEASVIPGSLGLLPSASLASLP----DTN-TAFGLY
GVLLADNTFGDMLSDQAGSIVGSLGVLPSASLSGIPGEKRKDGKKSALY
: : : . * . . * : : * * * . : * : : * : * : . * : : : . . .

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

EPTHGSAPTIAGKNIANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVL
EPIHGSAPDIAGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVI
EPIHGSAFDITGKGIANPVATFWTAAEMLEWLG-EKDAADKLMQCVCESVC
EPCHGSAPDLPAN-KVNPIATILSAASMLRLSLDCVKEAEAELEAVKQVL
EPTHGSAPT-----
** ****

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

DKGIRTSDLGGSTGTREFGDAVVAALKG
ESGVRTGDIGGKATTAEVGDAAAELE-
ESGILTADLGGTATTKEVTSVV-----
DSGIRTADLRGTSSTTEVGDAI-----

FIGURE 25

Identification of peptides in AFC fractions.

Protein extract	CssI (AnrP440134)	Hydrophobin (AnrP57221)	GAPDH (AnrP539502)	Enolase (AnrP7789)	Catalases and IMDH B
Diffusate	KVAQELINPGPK	FPVPDDITVK ATYAADVTDIDEGILAGTLK	AGISLNPFFVK TAAQNTIPSSFGAAK NILGYTEDDVVSSDLNGDER	NVNETIGPALIK VNQIGTLTESIQAAK TSDPQIVGDDLFTVTPGR	Not detected
Cell surface exposed	VAGELINPGPK	FPVPDDITVK ATYAADVTDIDEGILAGTLK	Not detected	Not detected	FGFDLLDPTK (Catalase B peptide AnrP977704) IX, AEX, ALR (IMDH B peptide)
Cell wall	KVAQELINPGPK VAGELINPGPK SISFQIDCR EGAEQSAAPQAEHSTK VVTTPYPCDQVK	FPVPDDITVK 3-12 ATYAADVTDIDEGILAGTLK 30-50	AGISLNPFFVK TAAQNTIPSSFGAAK NILGYTEDDVVSSDLNGDER VPTSNVSVVDLTCR YDTTHGQFK GTIEFYDQGLIVNGK	Not detected	TGPSLLEDQIAR (Catalase A peptide AnrP145557)
Peptides used for Ab production	KVAQELINPGPKVVT KEGAEGSAAPQAEHSTK	PVPDDITVKQATEKCGD ATYAADVTDIDEGIL	TEDDVVSSDLNGDERS FKGTIEFYDQGLIVNGK	KVNNETIGPALIKENID TSDPQIVGDDLFTVTPGR	DEEDQLRFGFDLLDPTKIIVP RIDNDLARRVARAIGV

FIGURE 26

Biochemical characteristics of Cssl.

	Complete	N-terminus	C-terminus
MW	28179.92	13960.38	14236.54
Residues	260	130	130
Strongly Basic (+) Amino Acids (K, R)	25	10	15
Strongly Acidic (-) Amino Acids (D, E)	33	9	24
Hydrophobic Amino Acids (A, I, L, F, W, V)	89	55	34
Polar Amino Acids (N, C, Q, S, T, Y)	70	36	34
Isoelectric Point	5.081	7.626	4.760
Charge at pH 7.0	-7.634	0.892	-8.617

FIGURE 27

Sequence of Polypeptides chosen for the production of multiple antigenic peptides and antisera against selected target proteins.

<u>Peptide name</u>	<u>Peptide sequence</u>	<u>Parental protein</u>	<u>Reactivity vs AfC*</u>	<u>Reactivity vs AfM*</u>
GAP-B-1	FKGTIETVDQGLVNGKK (SEQ ID NO:12)	GAPDH B	++	+++
GAP-B-2	TEDDVSSDLNGDERS (SEQ ID NO:11)	GAPDH B	+++	++
HYD-1	PVPDDITVKQATEKCGD (SEQ ID NO:9)	hydrophobin	++	+++
HYD-2	ATYAGDVTIDIEGL (SEQ ID NO:10)	hydrophobin	++	+
CAT-B-1	DEHDQLRFGFDLLDPTKIYP (SEQ ID NO:15)	Catalase B	++	++
CAT-B-2	RIDNDLARRVARAIGV (SEQ ID NO:16)	Catalase B	++	++
ENO-1	KNVNETTGPALIKENID (SEQ ID NO:13)	Enolase	++	-
ENO-2	TSDFOIVGDDLTVTNPGK (SEQ ID NO:14)	Enolase	-	+
Peptide 2	KEGAEQSAPQAEHSTK (SEQ ID NO:8)	CssI	+++	+++
Peptide 1	KVAQEINPGPKVVT (SEQ ID NO:7)	CssI	++	++

*Reactivity of sera raised against the peptide against the surface of AfC or AfM

FIGURE 28

Analysis of the ability of anti-IMDH B IgG to bind the surface of clinical isolates.

Strain Number	Original substratum	Pathogenicity (underlying disease):	Anti IMDH-B intensity	
			<u>Conidia</u>	<u>Mycelium</u>
Isolate 46640	Human Lung	Aspergilloma	++	++
IHEM 1246	Outdoor air	-----	+	+
IHEM 2494	Human sputum	Allergic Bronchopulmonar Aspergillosis	++	++
IHEM 2739	Human sinus	Mycotic sinusitis	++++	++
IHEM 2895	Human bronchoaspiration (fungal ball)	Bronchitis	+++	+
IHEM 3007	Human lung	Pulmonary aspergillosis	-	+++
IHEM 4184	Human lung biopsy	Aspergillosis (heart transplant)	-	++
IHEM 4185	Human bone	Aspergillosis (heart transplant)	-	++
IHEM 4187	Human bronchial secretions	Aspergillosis (liver transplant)	+	+
IHEM 4699	Human bronchoaspiration	Aspergillosis (bone marrow transplant)	++	+
IHEM 4750	Human lung from autopsy	Aspergillosis (liver transplant)	+++	ND
IHEM 4756	Human sputum	Aspergillosis (marrow transplant)	-	+

FIGURE 29

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